Genome Browser

Genome Browser under **Fine Genomes** is a way for selecting and browsing genomes in IMG.

Figure 1(i) shows the tree view of genomes in IMG. Please note that to include Viruses and GFragment (i.e., genome fragments), users will have to change the **Preferences** under **MyIMG**. The initial tree display only shows the domain level. Users can click on the "triangle" to expand to the phylum level as shown in Figure 1(ii). The process can be continued to class, order, etc. Users can also use "Open All" and "Close All" features to expand or close the tree expansion.
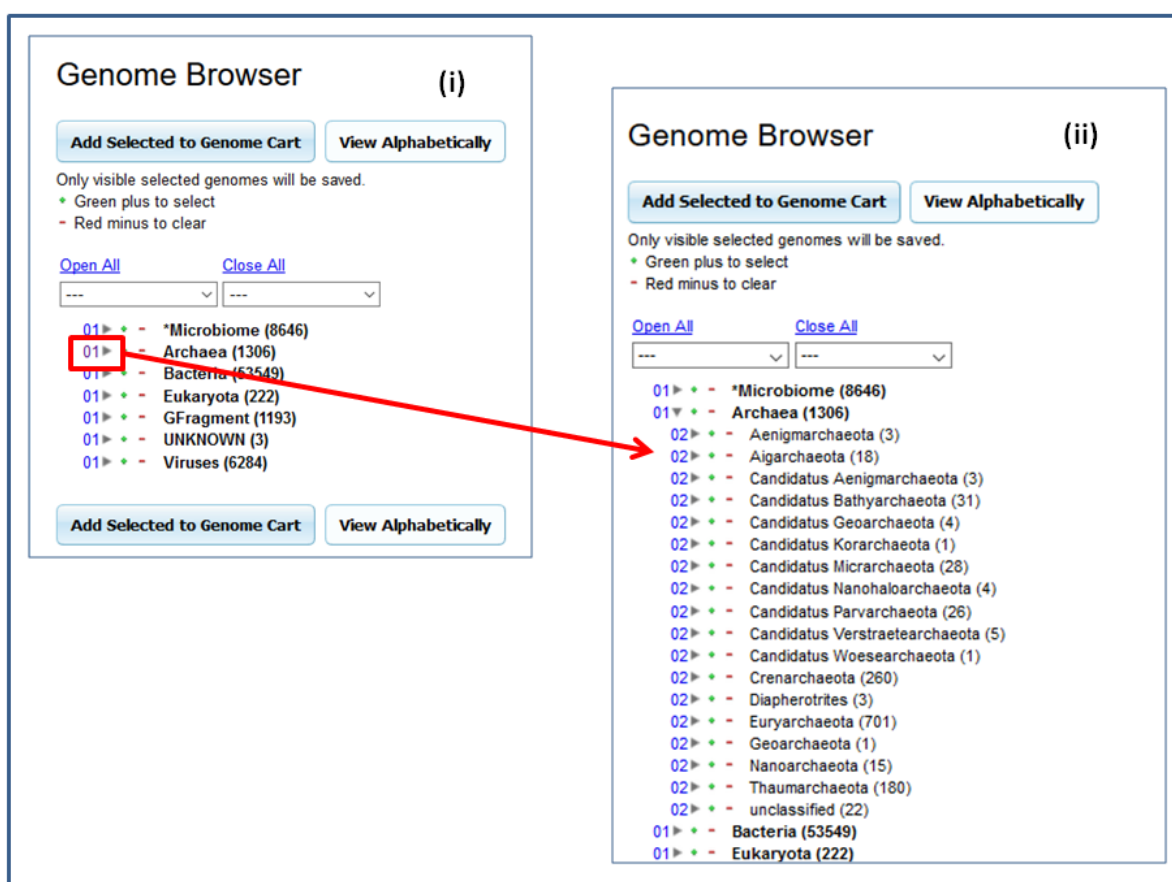

Figure 1. Genome Browser: Tree Display

To view genome list in a table format, simply click the **View Alphabetically** button (in Figure 1(i)). Figure 2 shows the table display of all genomes in IMG.

Figure 2. Genome Browser: Table Display

The **Genome Browser** allows user to select or de-select genomes individually or collectively. User can click on the name of an individual genome to view the associated Organism Details. User can also sort the alphabetical list of genomes by clicking on a column name. Alphabetical columns are sorted in ascending alphabetic order. Numeric columns are sorted in ascending numeric order.

 User can select genomes with the **Genome Browser** by clicking the checkbox next to each genome, and then clicking on **Add Selected to Genome Cart** button to save the genomes into Genome Cart. User also has the option to "Select All" of the genomes or "Clear All" of the selections.

Table Configuration

By default, the alphabetical list of genomes includes information on domain, sequencing status, study name, genome name, sequencing center, IMG Genome ID, genome size and gene count. However, user can configure the displayed columns by using the **Table Configuration** selector at the bottom of the **Gene Browser** page, as shown in Figure 3.

Figure 3. Table Configuration.

There are 3 categories of genome information:

1. *Genome Field*: Information regarding a genome such as phylogeny (phylum, class, ...), associated JGI and GOLD IDs, assembly method, etc.
2. *Metadata:* Genome associated metadata imported from GOLD (updated daily) such as altitude, latitude, culture type, ecosystem information, etc.
3. *Data Statistics*: Genome statistics information such as scaffold count, base count, gene count, etc. For metagenomes, there is an additional option to show assembled data, unassmebled data or both. (See the red rectangle near the upper right corner in Figure 3.)

Users will have to click the **Redisplay** button after any changes to the table configuration selection in order to view the changes.